

Fig. 1. Alignment of amino acid sequences of human $G\alpha_q$, $G\alpha_{15}$ and $G\alpha_{16}$ by Clustal method.

The matched residues are marked in shaded box. The sequence accession number in the GenBank database is AAB06875, P30678, and P30679 for h $G\alpha_q$, $G\alpha_{15}$, and $G\alpha_{16}$ respectively.

1	M T L E S I M A C C - - - L S E E A K E A R R I N D E I E R Q L R R D K R D A R	hGq
1	M A R S L T W G C C P W C L T E E E K T A A R I D Q E I N R I L L E Q K K Q E R	G15
1	M A R S L T W R C C P W C L T E D E K A A A R V D Q E I N R I L L E Q K K Q D R	G16
38	R E L K L L L L L G T G E S G K S T F I K Q M R I I H G S G Y S D E D K R G F T K	hGq
41	E E L K L L L L L G P G E S G K S T F I K Q M R I I H G V G Y S E E D R R A F R L	G15
41	G E L K L L L L L G P G E S G K S T F I K Q M R I I H G A G Y S E E E R K G F R P	G16
78	L V Y Q N I F T A M Q A M I R A M D T L K I P Y K Y E H N K A H A Q L V R E V D	hGq
81	L I Y Q N I F V S M Q A M I D A M D R L Q I P F S R P D S K Q H A S L V M T Q D	G15
81	L V Y Q N I F V S M R A M I E A M E R L Q I P F S R P E S K H H A S L V M S Q D	G16
118	V E K V S A F E N P Y V D A I K S L W N D P G I Q E C Y D R R R E Y Q L S D S T	hGq
121	P Y K V S T F E K P Y A V A M Q Y L W R D A G I R A C Y E R R R E F H L L D S A	G15
121	P Y K V T T F E K R Y A A A M Q W L W R D A G I R A C Y E R R R E F H L L D S A	G16
158	K Y Y L N D L D R V A D P A Y L P T Q Q D V L R V R V P T T G I I E Y P F D L Q	hGq
161	V Y Y L S H L E R I S E D S Y I P T A Q D V L R S R M P T T G I N E Y C F S V K	G15
161	V Y Y L S H L E R I T E E G Y V P T A Q D V L R S R M P T T G I N E Y C F S V Q	G16
198	S V I F R M V D V G G Q R S E R R K W I H C F E N V T S I M F L V A L S E Y D Q	hGq
201	K T K L R I V D V G G Q R S E R R K W I H C F E N V I A L I Y L A S L S E Y D Q	G15
201	K T N L R I V D V G G Q K S E R K K W I H C F E N V I A L I Y L A S L S E Y D Q	G16
238	V L V E S D N E N R M E E S K A L E R T I I T Y P W F Q N S S V I L F L N K K D	hGq
241	C L E E N D Q E N R M E E S L A L F S T I L E L P W F K S T S V I L F L N K T D	G15
241	C L E E N N Q E N R M K E S L A L F G T I L E L P W F K S T S V I L F L N K T D	G16
278	L L E E K I M Y S H L V D Y F P E Y D G P Q R D A Q A A R E F I L K M F V D L -	hGq
281	I L E D K I H T S H L A T Y F P S F Q G P R R D A E A A K S F I L D M Y A R V Y	G15
281	I L E E K I P T S H L A T Y F P S F Q G P K Q D A E A A K R F I L D M Y T R M Y	G16
317	- - - - N P D S D K I N - - - - Y S H F T C A T D T E N I R F V F A A V K	hGq
321	A S C A E P Q D G G R K G S R A R R F F A H F T C A T D T Q S V R S V F K D V R	G15
321	T G C V D G P E G S K K G A R S R R L F S H Y T C A T D T Q N I R K V F K D V R	G16
346	D T I L Q L N L K E Y N L V	hGq
361	D S V L A R Y L D E I N L L	G15
361	D S V L A R Y L D E I N L L	G16

Fig. 2. Amino acid sequences of the mouse and human $G\alpha_q$

1 = mouse
2 = human

1MTLESIMACCLSEEAKEARRINDEIER^QLRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGS^GYSDE
2MTLESIMACCLSEEAKEARRINDEIER^QLRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGS^GYSDE

DKRGFTKLVYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS^AFENPYVDAIKSLWNDPG
DKRGFTKLVYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS^AFENPYVDAIKSLWNDPG

IQECYDRRREYQLSDSTKY^YLNDLDRVADPSYLPTQ^QDVLRVRVPTTGII EYPFDLQSVIFRMVDVGGQR
IQECYDRRREYQLSDSTKY^YLNDLDRVADP^AYLPTQ^QDVLRVRVPTTGII EYPFDLQSVIFRMVDVGGQR

SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE

EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ

LNLKEYNLV
LNLKEYNLV

Key amino acids described in this invention are boxed
Difference between human and mouse is underlined

Fig. 3. Amino acid sequences of the mouse and human $G\alpha_q$ proteins tested. Variation of amino acids of $G\alpha_q$ is depicted in parenthesis. The sequence numbers of amino acid H or Q, V or L are 28 and 29 respectively. The sequence number of amino acid G or D is 66. Truncation of N-terminal six amino acids (MTLESI) are shown as ΔN . Hemagglutinin (HA) epitope tag (DVPDYA) spans from 125 to 130. C-terminal five amino acids (-t5) or 44 amino acids (-t44) of transducin and five amino acids of $G\alpha_{olf}$ (-olf5) are used respectively to replace those of $G\alpha_q$.

Mouse sequences created and tested:

Sequence ID#1

mGq

MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFENPYVDAIKSLWNDPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPSYLPTQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLV ALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#2

mGq (ΔN)

MACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFENPYVDAIKSLWNDPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPSYLPTQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLV ALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#3

mGq (HA)

MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPSYLPTQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLV ALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#4

mGq (ΔN -HA)

MACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPSYLPTQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLV ALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#5

mGq (ΔN -HVD-HA) from Kostenis et al 1998

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG

IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#6

mGq (ΔN-HVD-HA) -t5

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKDCGLF

Sequence ID#7

mGq (ΔN-HVD-HA) -t44

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDNMRRDVKEIYSHMTCATDTQNVKFV FDAVTDIIK
ENLKDCGLF

Sequence ID#8

mGq (ΔN-HVG-HA)

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#9

mGq (HVG-HA)

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#10

mGq (D-HA)

MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#11

mGq (HVD-HA)

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#12

mGq (HVG-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKDCGLF

Sequence ID#13

mGq (HVD-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKDCGLF

Sequence ID#14

mGq (ΔN-HVD-HA) -o1f5

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKQYELL

Human Sequences Tested

Sequence ID#15

hGq

MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFENPYVDAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNAV

Sequence ID#16

hGq (ΔN)

MACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFENPYVDAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR

SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
 EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
 LNLKEYNAV

Table I: Function Activity Of Gαq Variants Tested

Gq Variants	Seq ID #	Functional Activity with Taste Receptor mT2R5	Functional Activity with Olfactory Receptor mI7
mGq	1	-	Not tested
mGq(ΔN)	2	-	Not tested
mGq(HA)	3	-	Not tested
mGq(ΔN-HA)	4	-	Not tested
mGq(ΔN-HVD-HA)	5	+	+
mGq(ΔN-HVD-HA)-t5	6	++	Not tested
mGq(ΔN-HVD-HA)-t44	7	++	Not tested
mGq(ΔN-HV-HA)	8	-	Not tested
mGq(HV-HA)	9	-	Not tested
mGq(D-HA)	10	+	Not tested
mGq(HVD-HA)	11	+	Not tested
mGq(HV-HA)-t5	12	+	Not tested
mGq(HVD-HA)-t5	13	++	Not tested
mGq(ΔN-HVD-HA)-olf5	14	Not tested	++
hGq	15	-	Not tested
hGq(ΔN)	16	-	Not tested

+ means functionally couples with chemosensory receptor
 ++ means functionally couples with chemosensory receptor
 - means does not functionally couple

Figure 4. Other sequences predicted by this invention active in assays of chemosensory receptors such as those GPCRs involved in sensing of tastants, olfactants and pheromones.

Sequence ID#17

hGq (Δ N-HVD-HA)

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWN DPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPPTTGI IEYPFDLQSVI FRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#18

hGq (Δ N-HVD-HA) -t5

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWN DPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPPTTGI IEYPFDLQSVI FRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKDCGLF

Sequence ID#19

hGq (Δ N-HVD-HA) -t44

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWN DPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPPTTGI IEYPFDLQSVI FRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDNMRRDVKEIYSHMTCATDTQNVKFVFDVAVTDIIK
ENLKDCGLF

Sequence ID#20

hGq (D-HA)

MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWN DPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPPTTGI IEYPFDLQSVI FRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#21

hGq (HVD-HA)

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWN DPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPPTTGI IEYPFDLQSVI FRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#22

hGq (HVG-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKDCGLF

Sequence ID#23

hGq (HVD-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKDCGLF

Sequence ID#24

hGq (ΔN-HVD-HA) -o1f5

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKQYELL

Sequence ID#25

hGq (HVG-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKQYELL

Sequence ID#26

hGq (HVD-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY YLNDLDRVADPAYLPTQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKQYELL